Amendments to the Specification:

Please insert the following paragraph after the title on page 1 of the application:

CROSS REFERENCE TO RELATED APPLICATIONS

This application is a continuation of PCT Application No. PCT/CA00/0587, filed May 12, 2000, which claims priority from U.S. Provisional Application No. 60/134,259, filed May 14, 1999, the entire contents of both of which are hereby incorporated by reference.

Please replace the paragraph following the "Field of the Invention," with the following amended paragraph:

The present invention relates to ~~proteonomics~~ proteomics. More specifically, the invention relates to protein-protein interactions and methods for identifying interacting proteins and the amino acid sequence at the site of interaction.

Please replace the paragraph on page 21, lines 7-16, with the following amended paragraph:

Figure 5 shows a P-glycoprotein predicted secondary structure and amino acid of the linker domain. A schematic representation of ~~P-gp~~ the predicted secondary structure of P-gp. The twelve filled squares represent the twelve putative transmembrane domains. The two ATP binding domains are represented by two circles in the N- and C-terminal halves of P-gp. The inset represents the linker domain. The amino acid sequence of the linker domains of Human P-gp 1 (HP-gp1) and HP-gp3 is indicated as a single-letter amino acid code. The numbers in brackets at the beginning and end of each amino acid sequence of HP-gp1 **(SEQ ID NO: 15)** and HP-gp3 **(residues 1-89 of SEQ ID NO: 14)** shows the length of the linker domains (1 - 90 and [[1- 88]] 1-89 for HP-gp1 and HP-gp3, respectively). The numbered lines underneath the amino acid sequence show the sequences of the overlapping hexapeptides, which differ by one amino acid. For HP-gp3, the last hexapeptide is number [[88]] 89.